Soraya
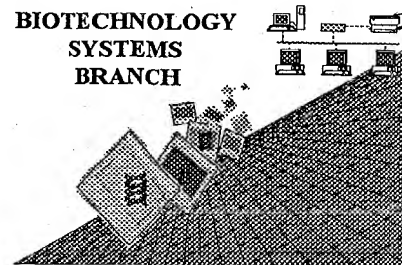
RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: *09/269250*

Art Unit / Team No. : *1655*

Date Processed by STIC: *2/29/2000*

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/269, 250_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This.may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

PP54

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

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 1   <110> APPLICANT: Goulmy, Els
 2   <120> TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN
 3         HA-1
 4   <130> FILE REFERENCE: 58994
 5   <140> CURRENT APPLICATION NUMBER: US/09/269,250
 6   <141> CURRENT FILING DATE: 1999-05-21
 7   <160> NUMBER OF SEQ ID NOS: 42
 8   <170> SOFTWARE: PatentIn Ver. 2.1
 9   <210> SEQ ID NO 1
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11   <212> TYPE: DNA
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16        gtggaagagg ccatgacagc taaggctctg agggatgtgt aggagtttgg tgggggagtc 180
17        cctgagcgta cactggctca agagggtgcc cactttattt tttttaaagg atctgatggc 240
18        aattaggagg gaaaggcaga ggaaatgtcc catgcacagg ctcagaaaca cggaaacaga 300
19        gaatgcattt ggggggccaag gtgtgggggtg ccgctggtgt aggatgaagg catgacaacg 360
20        ccaggcagaa gggcaat 377
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29   <210> SEQ ID NO 3
30   <211> LENGTH: 20
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32   <213> ORGANISM: Artificial Sequence
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37   <210> SEQ ID NO 4
38   <211> LENGTH: 20
39   <212> TYPE: DNA
40   <213> ORGANISM: Artificial Sequence
41   <220> FEATURE:
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43   <400> SEQUENCE: 4
44        tggctctcac cgtcacgcaa 20
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54    <211> LENGTH: 20
55    <212> TYPE: DNA
56    <213> ORGANISM: Artificial Sequence
57    <220> FEATURE:
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64    <213> ORGANISM: Artificial Sequence
65    <220> FEATURE:
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73    <220> FEATURE:
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81    <220> FEATURE:
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89    <220> FEATURE:
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93    <210> SEQ ID NO 11
94    <211> LENGTH: 18
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104    <213> ORGANISM: Artificial Sequence
105    <220> FEATURE:
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113    <220> FEATURE:
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207    <213> ORGANISM: HUMAN
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211    <211> LENGTH: 13
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216              1               5                   10
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229              1               5                   10
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241            Glu Cys Val Leu Arg Asp Asp Leu Leu Glu Ala Arg Arg
242              1               5                   10
243    <210> SEQ ID NO 31
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/269,250**

Input Set: **I269250.RAW**

Line	?	Error/Warning	Original Text
146	W	"N" or "Xaa" used: Feature required	Val Leu Xaa Asp Asp Leu Leu Glu Ala
286	W	"N" or "Xaa" used: Feature required	Tyr Xaa Thr Asp Arg Val Met Thr Val
295	W	"N" or "Xaa" used: Feature required	Val Xaa His Asp Asp Xaa Xaa Glu Ala